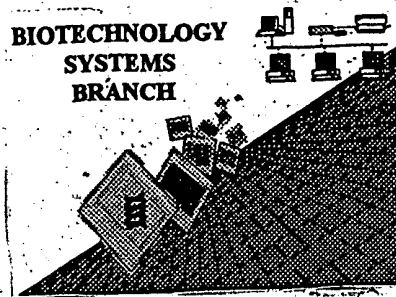


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING  
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/017,372  
Source: 01PE  
Date Processed by STIC: 1/2/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER  
VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>>), EFS Submission

User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/017,372

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length  
Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002  
TIME: 11:25:32

Input Set : A:\61302.ST25.txt  
Output Set: N:\CRF3\01022002\J017372.raw

*pp 1-3,5*  
**Does Not Comply  
Corrected Diskette Needed**

3 <110> APPLICANT: Wolfram, Lawrence  
4 Letterio, John  
6 <120> TITLE OF INVENTION: FUNCTIONALIZED TGF-BETA FUSION PROTEINS  
8 <130> FILE REFERENCE: 4239-61302  
10 <140> CURRENT APPLICATION NUMBER: US/10/017,372  
10 <141> CURRENT FILING DATE: 2001-10-19  
10 <150> PRIOR APPLICATION NUMBER: 60/242,292  
11 <151> PRIOR FILING DATE: 2000-10-20  
13 <160> NUMBER OF SEQ ID NOS: 39  
15 <170> SOFTWARE: PatentIn version 3.1  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 28  
19 <212> TYPE: DNA  
20 <213> ORGANISM: synthetic oligonucleotide *see item 10 on Eva Summary Sheet*  
22 <400> SEQUENCE: 1  
23 ggagagatct ggtaccgaga tggcgctt 28  
26 <210> SEQ ID NO: 2  
27 <211> LENGTH: 42  
28 <212> TYPE: DNA  
29 <213> ORGANISM: synthetic oligonucleotide  
31 <400> SEQUENCE: 2  
32 ataagaattg cggccgcttt aatcgatccc aagtgggctt gg 42  
35 <210> SEQ ID NO: 3  
36 <211> LENGTH: 48  
37 <212> TYPE: DNA  
38 <213> ORGANISM: synthetic oligonucleotide  
40 <400> SEQUENCE: 3  
41 gactacaagg atgacgacga caaggccctg gataccaact actgcttc 48  
44 <210> SEQ ID NO: 4  
45 <211> LENGTH: 45  
46 <212> TYPE: DNA  
47 <213> ORGANISM: synthetic oligonucleotide  
49 <400> SEQUENCE: 4  
50 cttgtcgtcg tcatccttgt agtctcggcg gtgccgggag ctgtg 45  
53 <210> SEQ ID NO: 5  
54 <211> LENGTH: 45  
55 <212> TYPE: DNA  
56 <213> ORGANISM: synthetic oligonucleotide  
58 <400> SEQUENCE: 5  
59 gactacaagg atgacgacga caggagaaga actgctgcgt gcggc 45  
62 <210> SEQ ID NO: 6  
63 <211> LENGTH: 45  
64 <212> TYPE: DNA  
65 <213> ORGANISM: synthetic oligonucleotide  
67 <400> SEQUENCE: 6  
68 cttgtcgtcg tcatccttgt agtctcggcg gtgccgggag ctgtg 45  
71 <210> SEQ ID NO: 7

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002

TIME: 11:25:32

Input Set : A:\61302.ST25.txt

Output Set: N:\CRF3\01022002\J017372.raw

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72 <211> LENGTH: 8
73 <212> TYPE: PRT
74 <213> ORGANISM: synthetic oligopeptide
76 <400> SEQUENCE: 7
78 Asp Tyr Lys Asp Asp Asp Asp Lys
79 1 5
82 <210> SEQ ID NO: 8
83 <211> LENGTH: 1197
84 <212> TYPE: DNA
85 <213> ORGANISM: fusion
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (1)..(1197)
90 <223> OTHER INFORMATION:
93 <220> FEATURE:
94 <221> NAME/KEY: misc_feature
95 <222> LOCATION: (278)..(279)
96 <223> OTHER INFORMATION: Maturation cleavage site
99 <400> SEQUENCE: 8
100 atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg ccg ctg ctg 48
101 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
102 1 5 10 15
104 tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc 96
105 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
106 20 25 30
108 tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 144
109 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
110 35 40 45
112 att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc 192
113 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
114 50 55 60
116 cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt 240
117 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
118 65 70 75 80
120 tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag 288
121 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
122 85 90 95
124 ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta 336
125 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
126 100 105 110
128 atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc 384
129 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
130 115 120 125
132 cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg 432
133 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
134 130 135 140
136 ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc 480
137 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
138 145 150 155 160

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002

TIME: 11:25:32

Input Set : A:\61302.ST25.txt

Output Set: N:\CRF3\01022002\J017372.raw

```

140 aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat      528
141 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
142                               165                               170                               175
144 gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca      576
145 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
146                               180                               185                               190
148 ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg      624
149 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
150                               195                               200                               205
152 acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc      672
153 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
154                               210                               215                               220
156 tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat      720
157 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
158 225                               230                               235                               240
160 tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc      768
161 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
162                               245                               250                               255
164 ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag cac ctg cac      816
165 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
166                               260                               265                               270
168 agc tcc cgg cac cgc cga gac tac aag gat gac gac gac aag gcc ctg      864
169 Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
170                               275                               280                               285
172 gat acc aac tac tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg      912
173 Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
174                               290                               295                               300
176 cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat      960
177 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
178 305                               310                               315                               320
180 gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac      1008
181 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
182                               325                               330                               335
184 atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac      1056
185 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
186                               340                               345                               350
188 cag cac aac ccg ggc gcg tgc gcg gcg ccg tgc tgc gtg ccg cag gcg      1104
189 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
190                               355                               360                               365
192 ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg      1152
193 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
194                               370                               375                               380
196 gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga      1197
197 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
198 385                               390                               395
201 <210> SEQ ID NO: 9
202 <211> LENGTH: 398
203 <212> TYPE: PRT
204 <213> ORGANISM: fusion

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002  
 TIME: 11:25:32

Input Set : A:\61302.ST25.txt  
 Output Set: N:\CRF3\01022002\J017372.raw

206 <220> FEATURE:  
 207 <221> NAME/KEY: misc\_feature  
 208 <222> LOCATION: (278)..(279)  
 209 <223> OTHER INFORMATION: Maturation cleavage site  
 211 <400> SEQUENCE: 9  
 213 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu  
 214 1 5 10 15  
 217 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr  
 218 20 25 30  
 221 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala  
 222 35 40 45  
 225 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser  
 226 50 55 60  
 229 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu  
 230 65 70 75 80  
 233 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu  
 234 85 90 95  
 237 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu  
 238 100 105 110  
 241 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro  
 242 115 120 125  
 245 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val  
 246 130 135 140  
 249 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu  
 250 145 150 155 160  
 253 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn  
 254 165 170 175  
 257 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser  
 258 180 185 190  
 261 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu  
 262 195 200 205  
 265 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser  
 266 210 215 220  
 269 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn  
 270 225 230 235 240  
 273 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro  
 274 245 250 255  
 277 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His  
 278 260 265 270  
 281 Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu  
 282 275 280 285  
 285 Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg  
 286 290 295 300  
 289 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His  
 290 305 310 315 320  
 293 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr  
 294 325 330 335  
 297 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn  
 298 340 345 350

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002  
TIME: 11:25:32

Input Set : A:\61302.ST25.txt  
Output Set: N:\CRF3\01022002\J017372.raw

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301 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
302          355          360          365
305 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
306          370          375          380
309 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
310 385          390          395
313 <210> SEQ ID NO: 10
314 <211> LENGTH: 362
315 <212> TYPE: DNA
316 <213> ORGANISM: fusion
318 <400> SEQUENCE: 10
319 gactacaagg atgacgacga caaggccctg gataccaact actgcttcag ctccacggag      60
321 aagaactgct gcgtagcgga gctctacatt gacttcggga aggacctggg ctggaagtgg      120
323 attcatgaac ccaagggtc catgccaatt tctgacctgg gccctgtccc tacatctgga      180
325 gcctagacac tcagtacagc aaggtcctgg ctctgtacaa ccagcacaac ccgggcgcgt      240
327 cggcggcgcc gtgctgcgtg ccgcaggcgc tggagccact gcccatcgtg tactacgtgg      300
329 gccgcaagcc caaggtggag cagctgtcca acatgatcgt gcgttcctgc aagtgcagct      360
331 ga
334 <210> SEQ ID NO: 11
335 <211> LENGTH: 120
336 <212> TYPE: PRT
337 <213> ORGANISM: fusionprotein
339 <220> FEATURE:
340 <221> NAME/KEY: PEPTIDE
341 <222> LOCATION: (1)..(8)
342 <223> OTHER INFORMATION: FLAG tag
345 <400> SEQUENCE: 11
347 Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe
348 1          5          10          15
351 Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe
352          20          25          30
355 Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
356          35          40          45
359 Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
360          50          55          60
363 Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
364 65          70          75          80
367 Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
368          85          90          95
371 Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
372          100          105          110
375 Ile Val Arg Ser Cys Lys Cys Ser
376          115          120
379 <210> SEQ ID NO: 12
380 <211> LENGTH: 1197
381 <212> TYPE: DNA
382 <213> ORGANISM: fusion
384 <220> FEATURE:
385 <221> NAME/KEY: CDS

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*Please correct this error in  
subsequent sequences*

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/017,372

DATE: 01/02/2002

TIME: 11:25:33

Input Set : A:\61302.ST25.txt

Output Set: N:\CRF3\01022002\J017372.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date